

10/538201

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,201
Source: PG
Date Processed by STIC: 4/14/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/14/2006

PATENT APPLICATION: US/10/538,201

TIME: 11:30:18

Input Set : A:\4-32761A_UNZ.ST25.txt

Output Set: N:\CRF4\04142006\J538201.raw

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3 <110> APPLICANT: Novartis AG
5 <120> TITLE OF INVENTION: Organic Compound
7 <130> FILE REFERENCE: 4-32761P1/UNZ
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/538,201
C--> 9 <141> CURRENT FILING DATE: 2006-03-08
9 <160> NUMBER OF SEQ ID NOS: 44
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 18
15 <212> TYPE: PRT
16 <213> ORGANISM: Rattus norvegicus
18 <220> FEATURE:
19 <221> NAME/KEY: PEPTIDE
20 <222> LOCATION: (1)..(18)
21 <223> OTHER INFORMATION: rat NogoA_623-640
24 <400> SEQUENCE: 1
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27 1          5          10          15
30 Glu Ala
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35 <211> LENGTH: 221
36 <212> TYPE: PRT
37 <213> ORGANISM: Mus musculus
39 <220> FEATURE:
40 <221> NAME/KEY: CHAIN
41 <222> LOCATION: (1)..(221)
42 <223> OTHER INFORMATION: Variable part of Heavy Chain of 11C7 with leader sequence
45 <400> SEQUENCE: 2
47 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
48 1          5          10          15
51 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
52          20          25          30
55 Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
56          35          40          45
59 Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
60          50          55          60
63 Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
64 65          70          75          80
67 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
68          85          90          95
71 Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
72          100         105         110
75 Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln

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76          115          120          125
79 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
80          130          135          140
83 Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
84 145          150          155          160
87 Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
88          165          170          175
91 Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
92          180          185          190
95 Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
96          195          200          205
99 Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
100          210          215          220
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 238
105 <212> TYPE: PRT
106 <213> ORGANISM: Mus musculus
108 <220> FEATURE:
109 <221> NAME/KEY: CHAIN
110 <222> LOCATION: (1)..(238)
111 <223> OTHER INFORMATION: Light Chain of 11C7 with leader sequence
114 <400> SEQUENCE: 3
116 Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
117 1          5          10          15
120 Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile
121          20          25          30
124 Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
125          35          40          45
128 Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
129          50          55          60
132 Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
133 65          70          75          80
136 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
137          85          90          95
140 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
141          100          105          110
144 Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
145          115          120          125
148 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
149          130          135          140
152 Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
153 145          150          155          160
156 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
157          165          170          175
160 Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
161          180          185          190
164 Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
165          195          200          205
168 Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr

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169      210      215      220
172 Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys
173 225      230      235
176 <210> SEQ ID NO: 4
177 <211> LENGTH: 3919
178 <212> TYPE: DNA
179 <213> ORGANISM: Homo sapiens
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (1)..(3579)
184 <223> OTHER INFORMATION: Human NogoA
187 <400> SEQUENCE: 4
188 atg gaa gac ctg gac cag tct cct ctg gtc tcg tcc tcg gac agc cca      48
189 Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
190 1      5      10      15
192 ccc cgg ccg cag ccc gcg ttc aag tac cag ttc gtg agg gag ccc gag      96
193 Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
194      20      25      30
196 gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac      144
197 Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
198      35      40      45
200 ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc      192
201 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
202      50      55      60
204 gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac      240
205 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
206 65      70      75      80
208 ttc gga aat gac ttc gtg ccg ccg gcg ccc cgg gga ccc ctg ccg gcc      288
209 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
210      85      90      95
212 gct ccc ccc gtc gcc ccg gag ccg cag ccg tct tgg gac ccg agc ccg      336
213 Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
214      100      105      110
216 gtg tcg tcg acc gtg ccc gcg cca tcc ccg ctg tct gct gcc gca gtc      384
217 Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Val
218      115      120      125
220 tcg ccc tcc aag ctc cct gag gac gac gag cct ccg gcc cgg cct ccc      432
221 Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
222      130      135      140
224 cct cct ccc ccg gcc agc gtg agc ccc cag gca gag ccc gtg tgg acc      480
225 Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
226 145      150      155      160
228 ccg cca gcc ccg gct ccc gcc gcg ccc ccc tcc acc ccg gcc gcg ccc      528
229 Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
230      165      170      175
232 aag cgc agg ggc tcc tcg ggc tca gtg gat gag acc ctt ttt gct ctt      576
233 Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
234      180      185      190
236 cct gct gca tct gag cct gtg ata cgc tcc tct gca gaa aat atg gac      624

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237	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Arg	Ser	Ser	Ala	Glu	Asn	Met	Asp	
238			195					200					205				
240	ttg	aag	gag	cag	cca	ggt	aac	act	att	tcg	gct	ggt	caa	gag	gat	ttc	672
241	Leu	Lys	Glu	Gln	Pro	Gly	Asn	Thr	Ile	Ser	Ala	Gly	Gln	Glu	Asp	Phe	
242			210				215					220					
244	cca	tct	gtc	ctg	ctt	gaa	act	gct	gct	tct	ctt	cct	tct	ctg	tct	cct	720
245	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser	Leu	Ser	Pro	
246	225						230					235				240	
248	ctc	tca	gcc	gct	tct	ttc	aaa	gaa	cat	gaa	tac	ctt	ggt	aat	ttg	tca	768
249	Leu	Ser	Ala	Ala	Ser	Phe	Lys	Glu	His	Glu	Tyr	Leu	Gly	Asn	Leu	Ser	
250					245					250				255			
252	aca	gta	tta	ccc	act	gaa	gga	aca	ctt	caa	gaa	aat	gtc	agt	gaa	gct	816
253	Thr	Val	Leu	Pro	Thr	Glu	Gly	Thr	Leu	Gln	Glu	Asn	Val	Ser	Glu	Ala	
254			260					265					270				
256	tct	aaa	gag	gtc	tca	gag	aag	gca	aaa	act	cta	ctc	ata	gat	aga	gat	864
257	Ser	Lys	Glu	Val	Ser	Glu	Lys	Ala	Lys	Thr	Leu	Leu	Ile	Asp	Arg	Asp	
258			275				280						285				
260	tta	aca	gag	ttt	tca	gaa	tta	gaa	tac	tca	gaa	atg	gga	tca	tcg	ttc	912
261	Leu	Thr	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	Gly	Ser	Ser	Phe	
262			290				295					300					
264	agt	gtc	tct	cca	aaa	gca	gaa	tct	gcc	gta	ata	gta	gca	aat	cct	agg	960
265	Ser	Val	Ser	Pro	Lys	Ala	Glu	Ser	Ala	Val	Ile	Val	Ala	Asn	Pro	Arg	
266	305					310					315					320	
268	gaa	gaa	ata	atc	gtg	aaa	aat	aaa	gat	gaa	gaa	gag	aag	tta	gtt	agt	1008
269	Glu	Glu	Ile	Ile	Val	Lys	Asn	Lys	Asp	Glu	Glu	Glu	Lys	Leu	Val	Ser	
270					325					330				335			
272	aat	aac	atc	ctt	cat	aat	caa	caa	gag	tta	cct	aca	gct	ctt	act	aaa	1056
273	Asn	Asn	Ile	Leu	His	Asn	Gln	Gln	Glu	Leu	Pro	Thr	Ala	Leu	Thr	Lys	
274				340					345				350				
276	ttg	gtt	aaa	gag	gat	gaa	gtt	gtg	tct	tca	gaa	aaa	gca	aaa	gac	agt	1104
277	Leu	Val	Lys	Glu	Asp	Glu	Val	Val	Ser	Ser	Glu	Lys	Ala	Lys	Asp	Ser	
278			355				360						365				
280	ttt	aat	gaa	aag	aga	gtt	gca	gtg	gaa	gct	cct	atg	agg	gag	gaa	tat	1152
281	Phe	Asn	Glu	Lys	Arg	Val	Ala	Val	Glu	Ala	Pro	Met	Arg	Glu	Glu	Tyr	
282			370				375					380					
284	gca	gac	ttc	aaa	cca	ttt	gag	cga	gta	tgg	gaa	gtg	aaa	gat	agt	aag	1200
285	Ala	Asp	Phe	Lys	Pro	Phe	Glu	Arg	Val	Trp	Glu	Val	Lys	Asp	Ser	Lys	
286	385					390					395					400	
288	gaa	gat	agt	gat	atg	ttg	gct	gct	gga	ggt	aaa	atc	gag	agc	aac	ttg	1248
289	Glu	Asp	Ser	Asp	Met	Leu	Ala	Ala	Gly	Gly	Lys	Ile	Glu	Ser	Asn	Leu	
290					405					410				415			
292	gaa	agt	aaa	gtg	gat	aaa	aaa	tgt	ttt	gca	gat	agc	ctt	gag	caa	act	1296
293	Glu	Ser	Lys	Val	Asp	Lys	Lys	Cys	Phe	Ala	Asp	Ser	Leu	Glu	Gln	Thr	
294				420					425				430				
296	aat	cac	gaa	aaa	gat	agt	gag	agt	agt	aat	gat	gat	act	tct	ttc	ccc	1344
297	Asn	His	Glu	Lys	Asp	Ser	Glu	Ser	Ser	Asn	Asp	Asp	Thr	Ser	Phe	Pro	
298			435				440						445				
300	agt	acg	cca	gaa	ggt	ata	aag	gat	cgt	tca	gga	gca	tat	atc	aca	tgt	1392
301	Ser	Thr	Pro	Glu	Gly	Ile	Lys	Asp	Arg	Ser	Gly	Ala	Tyr	Ile	Thr	Cys	

DATE: 04/14/2006

TIME: 11:30:18

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/538,201

DATE: 04/14/2006

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Input Set : A:\4-32761A_UNZ.ST25.txt

Output Set: N:\CRF4\04142006\J538201.raw

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2074 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:2071